Multivariable system identification for dynamic discrete-time nonlinear system using genetic algorithm

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A. *Abstract* – Model structure selection based on genetic algorithm, which was originally derived for single-input single-output (SISO) systems, is extended to multi-input multi-output (MIMO) dynamic discrete-time nonlinear systems. This paper studies the algorithm in identifying the model structure for a jacketed continuous stirred tank reactor or CSTR. The adequacy of the developed model is tested using one step ahead prediction and cross validation test.

Keywords: **system identification, model structure selection, multivariable system, genetic algorithm**

I. INTRODUCTION

In system identification, a mathematical model is derived so that this model is able to simulate and predict the actual system behavior. The main problem in system identification is choosing the proper structure of the model where the significant terms are selected in the final model among all the possible ones. A polynomial Nonlinear AutoRegressive Moving Average with exogenous input or NARMAX model representation was selected as the model representation in this study since it has been shown to represent a wide range of nonlinear systems [1]. This model has received more research attention than other models such as block oriented models and functional series expansion model [2] due to its advantage such as having a linear-in-the-parameter model. The number of possible terms in AutoRegressive Moving Average with eXogenous input or ARMAX model is equal to the sum of allowable maximum lags while the maximum number of terms in NARMAX model is enormously large [3], therefore it is important to select the significant terms for the model that will produce a parsimonious model that adequately represents the data set. Billings and Fadzil [4] have showed that less than ten terms in NARMAX model are sufficient provided that the significant terms in the model can be detected. Several model structure selection methods have been derived for SISO nonlinear system using different methods such as orthogonal least square or OLS [5] which select the significant terms based on Error Reduction or *ERR*. However, higher order of input and output lags and higher order of nonlinearity will lead to a large searching space and high computation.

Recently, extensive work on genetic algorithm has been reported covering various applications. It is a search procedure that imitates the principle of natural evolution and it has received significant interest to researchers and has been applied to various optimization problems [6]. It offers many advantages such as having global search characteristics [7] and this has led to the idea of using this type of programming method in modeling of dynamical systems [8,9]. The algorithm starts with a randomly generated population and followed with three basic operators: reproduction, crossover and mutation. Most of those methods (OLS and GA) were applied to identification of SISO nonlinear systems and can be extended to MIMO system. There were applications of GA in MIMO systems hower using ARMAX model representation [10,11] and GA was used to calculate parameters of the models.

In this work, genetic algorithm is applied to the identification of multivariable dynamic discrete-time nonlinear system and the paper is organized as follows. In section 2, a background on multivariable system is discussed which will be used as the basis for the identification. In section 3, the proposed model structure selection using genetic algorithm is presented. Section 4 shows the application of the algorithm to a jacketed CSTR system. Some simulation results are presented in this section. The conclusion discusses and summarizes the main contribution of the paper.

II. IDENTIFICATION OF MULTIVARIABLE SYSTEM

A. System Representation

For a linear multivariable system with m outputs and n inputs, consider the ARMAX model below:

$$A(q^{-1})y(t) = B(q^{-1})u(t) + e(t) \qquad (1)$$

where $A(q^{-1})$ and $B(q^{-1})$ are the matrix polynomials of dimension (m x m) and (m x n) respectively as follows:

$$A(q^{-1}) = 1 + A_1 q^{-1} + A_2 q^{-2} + \ldots + A_{n_y} q^{-n_y}$$

$$B(q^{-1}) = B_1 q^{-1} + B_2 q^{-2} + \ldots + B_{n_u} q^{-n_u} \qquad (2)$$

The model belongs to linear-in-the-parameter model therefore, the parameter estimation can be performed using least square method. The model in equation (1) can be represented as [12]

$$y(t) = \phi^T(t)\theta + e(t) \qquad (3)$$

with

$$\phi^T(t) = \begin{pmatrix} \varphi^T(t) & 0 & \\ & \ddots & \\ & & \\ 0 & & \varphi^T(t) \end{pmatrix} \quad (4a)$$

$$\varphi^T(t) = (y^T(t-1)...y^T(t-n_y)u^T(t-1)... \\ u^T(t-n_u)) \quad (4b)$$

$$\theta = \begin{pmatrix} \theta^1 \\ \vdots \\ \theta^{ny} \end{pmatrix} \quad (4c)$$

Alternatively, Billings *et al.* [13] described a discrete-time multivariable nonlinear system with m outputs and n inputs by the model

$$y(t) = f(y(t-1),...,y(t-n_y),u(t-1),..., \\ u(t-n_u),e(t-1),...,e(t-n_y)) + e(t) \quad (5)$$

where

$$y(t) = \begin{pmatrix} y_1(t) \\ \vdots \\ y_m(t) \end{pmatrix}, \quad u(t) = \begin{pmatrix} u_1(t) \\ \vdots \\ u_n(t) \end{pmatrix}, \quad e(t) = \begin{pmatrix} e_1(t) \\ \vdots \\ e_m(t) \end{pmatrix}$$

For ith row, with different maximum lags for each output, input and noise, the equation can be written as

$$y_i(t) = f_i(y_1(t-1),...,y_1(t-n^i_{y_1}),...,y_m(t-1),...,y_m(t-n^i_{y_m}), \\ u_1(t-1),...,u_1(t-n^i_{u_1}),...,u_n(t-1),...,u_n(t-n^i_{u_n}), \\ e_1(t-1),...,e_1(t-n^i_{e_1}),...,e_m(t-1),...,e_m(t-n^i_{e_m})) \\ e_i(t)\ ,\ i = 1,...,m \quad (6)$$

where f_i is the nonlinear function.

If the polynomial degree for the ith subsystem model is L_i, the number of maximum terms for the ith subsystem model is

$$n_i = \sum_{j=0}^{L_i} n_{ij}, \quad (7)$$

where $$n_{ij} = \frac{n_{ij-1}\left[\sum_{k=1}^{m}(n^i_{y_k} + n^i_{e_k}) + \sum_{k=1}^{r} n^i_{u_k} + j - 1\right]}{j},$$

and $n_{i0} = 1, j = 1, \ldots, L_i$

B. Model validation

Model validation is the final step in system identification procedure to check whether the identified model sufficiently described the system based on the observed data. There are a number of ways to test the models. One of the most common methods is one step-ahead prediction which is used as a measure of the predictive accuracy of the identified model.

The one step-ahead prediction (OSA) of $\hat{y}_i(t)$ is defined as

$$\hat{y}_i(t) = \hat{F}_i(y_1(t-1),...,y_1(t-n^i_{y_1}),...,y_m(t-1),...,y_m(t-n^i_{y_m}), \\ u_1(t-1),...,u_1(t-n^i_{u_1}),...,u_n(t-1),...,u_n(t-n^i_{u_n}), \\ e_1(t-1),...,e_1(t-n^i_{e_1}),...,e_m(t-1),...,e_m(t-n^i_{e_m})) \quad (8)$$

where the predicted output is based on the previous input and output data. $\hat{F}_i(t)$ is an estimate of the nonlinear function $f_i(.)$.

In cross validation test, the parameter estimates are determined from the first data set and then the model output is computed for the different sets of data using the parameter estimates obtained from the first data set. The goodness of fit of the identified model is evaluated by comparing the system output $y_i(t)$ and the one-step-ahead prediction output $\hat{y}_i(t)$ and plotting on the same graph.

The performance of the model is also evaluated using Error Index (*EI*) defined as

$$EI = \sqrt{\frac{\sum (y(t) - \hat{y}(t))^2}{\sum y^2(t)}} \quad (9)$$

where the measure of closeness between the predicted output and the measure output is calculated.

III. MODEL STRUCTURE SELECTION USING GENETIC ALGORITHM

The main issue in identifying NARMAX model is the selection of the significant terms to represent the system. GA is used to select the significant terms based on its objective function. The algorithm starts with a randomly generated population. The three basic operations in GA (reproduction, crossover and mutation) are repeatedly applied to the population until an acceptable solution is found. In reproduction, individuals with higher objective function will more likely to produce offspring to the next generation through the survival of fittest mechanism. The method used is roulette wheel selection and this concept is extended to multivariable system.

The algorithm developed for identifying multivariable nonlinear system in this study is shown in Figure 1 and can be summarized below.

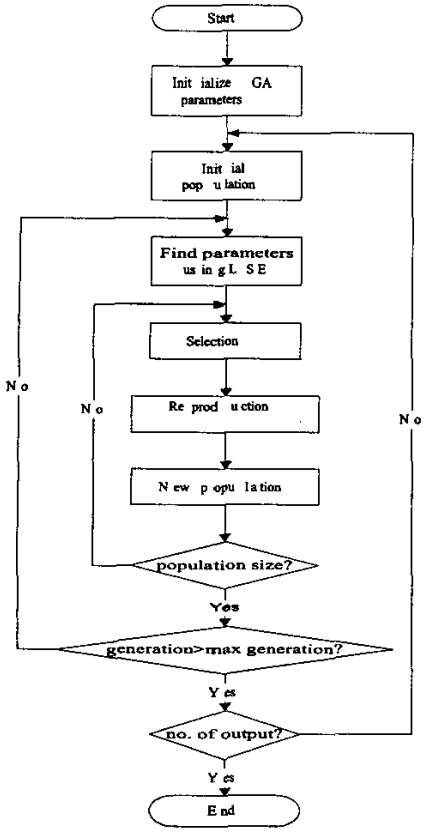

Figure 1 Procedure for identification of multivariable system using genetic algorithm

- *Initialization of GA control parameters*
  A population size, the probability for crossover (p_c) and mutation (p_m), stopping criterion are chosen as well as the maximum number of terms for the model.
- *Representation*
  The individual or chromosome represents the model structure, therefore each bit of the chromosome represents the term for the regressor in the equation. It consists of L-bit binary code and the length of L equals the size of regressor.
- *Initial population*
  Initially, m individuals are created at random. Each individual that represents a possible model is expressed by L-bit binary model code c. If some bits of the binary model of chromosome c equals zeros, it means the terms are excluded from the model

- *Parameter estimation* θ_i
  The selected term for the model is given by value 1 of each chromosome. Based on the identified model structure, the value of the parameters θ_i are calculated using the least square estimation method.
- *Fitness function*
  The objective of the algorithm is to minimize the error between the model and the system.
- *Reproduction*
  The new generation is produced using three basic GA operators: selection, crossover and mutation
- *Stopping criteria*
  After a stopping criteria has been met (specified number of generation, maximum number of outputs), the final models will be selected based on the models with maximum number of fitness value.

IV. SIMULATION STUDIES

A perfectly mixed, single first-order exothermic irreversible continuous stirred tank reactor (CSTR) [14] is used to represent a common multivariable nonlinear system in this study. The CSTR is a rather common process in the chemical industries. There are 274 of input and output data with the input $u(t)$ is the coolant jacket temperature set point while the output $y_1(t)$ is the reactor temperature and $y_2(t)$ is the reactant concentration. For simplicity, few assumptions are being made: (a) the coolant jacket temperature, T_j is directly manipulated to control the CSTR temperature (b) both the CSTR and coolant jacket are perfectly well stirred and the temperatures are distributed uniformly and T_j responses instantaneously when different set points of coolant jacket temperature are set (c) constant physical properties of inlet and outlet streams. The process can be described by the ordinary differential equation (ODE) showing the energy balance as in equation (10) and the mass balance as in (11)

The change in simulated reactant concentration is given by

$$\frac{dC_a}{dt} = \frac{F}{V}(C_{af} - C_a) - k_0 \exp\left(\frac{-\Delta E}{RT}\right) C_a \tag{10}$$

The change in reactor temperature is given by

$$\frac{dT}{dt} = \frac{F}{V}(T_f - T) + \left(\frac{-\Delta H}{\rho C_p}\right) k_0 \exp\left(-\frac{E}{RT}\right) C_a - \left(\frac{UA}{V\rho C_p}\right)(T - T_c) \tag{11}$$

In this study, genetic algorithm is used to identify a nonlinear system based on NARMAX model structure with $n_{y1} = n_{y2} = 2$, $n_u = 2$ and the nonlinearity l is equal to 2. The maximum number of model terms is 14 and there are 16,384 possible models to be selected from. The parameters used in the algorithms are 50, 0.6 and 0.01 for population size, p_c and p_m respectively. After 100 generation, the GA yields the following model as given on Table 1 and the values of error index for both outputs are given. The numbers of terms are 10 for model output 1 and 11 for model output 2. The system outputs superimposed with model outputs as well as the modeling residuals are shown in Figures 2, 3, 4 and 5. These

graphs show the algorithm provides a good performance and both of the two models have good accuracy.

To further validate the models, two different sets of data containing 258 and 355 data sets were applied to the identified model and the responses are shown in Figure 6, 7, 8 and 9. In order to give a quantitative measurement, the values of *IE* for those models are calculated. The values are 0.0034 for model output 1, 6.1177e-04 for model output 2 using the second data set, 0.0029 for model output 1 and 4.8332e-004 for model output 2 using the third data set. These validation results show that the algorithm gives excellent performance and both models provide good approximations for the multivariable nonlinear system.

V. DISCUSSION AND CONCLUSION

The study has focused on model structure selection for linear-in-the-parameters multivariable dynamic nonlinear systems using genetic algorithms. It is shown that the proposed algorithm provides an efficient way of determining the model structure of unknown nonlinear systems. Least square estimate was used in the parameter estimation as it is a widely used method and provides an efficient way of estimating the parameters on the models. The results obtained in this work indicate that the algorithm is capable of determining model structure of unknown nonlinear dynamic system with less number of terms. The results also showed that the proposed algorithm is able to accurately identify the models with a faster convergence rate. The one step-ahead-prediction of the models are plotted and the models are tested with cross validation tests. The validation tests have all shown good results and the values of error index are provided.

However, there are some limitations of the GA that was discovered in the work such as the premature convergence of the GA and the lack the hill-climbing characteristics. To enhance the genetic search, different authors proposed different approaches [15]. A study on the influence of the control parameters on genetic search was presented. The results suggested that (a) larger population size will improve the search but it will take longer time to converge (b) a good combination of genetic operators such as crossover and mutation is important and therefore good choice of these combination is needed by trial and error method so that better results can be achieved. To further improve the search, the simple GA needs to be modified. Further investigation on modified GA will be presented in the future.

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Table 1 Model structure for jacketed CSTR using ga

Sub-system	Terms	Estimates	Error Index
1	$y_1(t\text{-}2)$	-35.6399	0.0031
	u(t-2)	-0.0151	
	$y_1^2(t\text{-}1)$	-0.1927	
	$y_1(t\text{-}1)^* y_1(t\text{-}2)$	0.3439	
	$y_1(t\text{-}1)^* u(t\text{-}1)$	0.0391	
	$y_1(t\text{-}2)^* y_2(t\text{-}1)$	1.0537	
	$y_1(t\text{-}2)^* u(t\text{-}1)$	-0.0271	
	$y_2(t\text{-}1)^* y_2(t\text{-}2)$	-3.2639	
	$y_2^2(t\text{-}2)$	3.5853	
	u^2(t-1)	-0.0060	
2	$y_1(t\text{-}1)$	-6.9942	4.3087e-4
	u(t-1)	12.9807	
	$y_1(t\text{-}1)^* y_2(t\text{-}1)$	-0.0735	
	$y_1(t\text{-}1)^* y_2(t\text{-}2)$	0.3707	
	$y_1(t\text{-}1)^* u(t\text{-}1)$	-0.0088	
	$y_1^2(t\text{-}2)$	0.0084	
	$y_1(t\text{-}2)^* u(t\text{-}1)$	-0.0220	
	$y_1(t\text{-}2)^* u(t\text{-}2)$	-0.0006	
	$y_2(t\text{-}1)^* u(t\text{-}2)$	0.0014	
	$y_2(t\text{-}2)^* u(t\text{-}1)$	-0.4829	
	u^2(t-1)	0.0008	

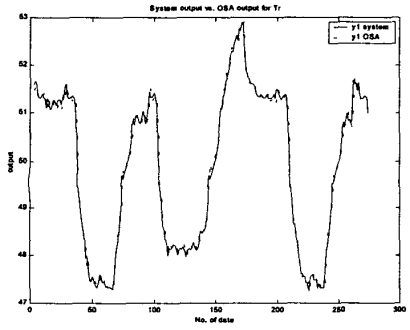

Figure 2 System output $y_1(t)$ versus predicted output

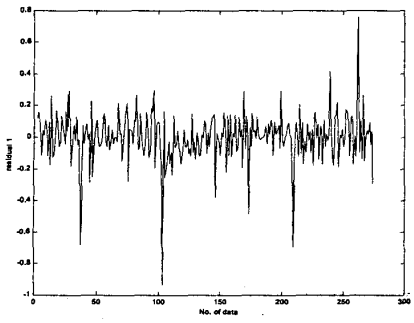

Figure 3 Residual e_1

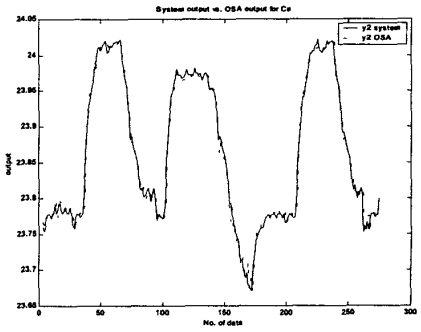

Figure 4 System output $y_2(t)$ versus predicted output

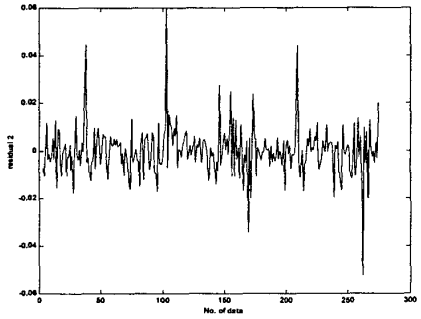

Figure 5 Residual e_2

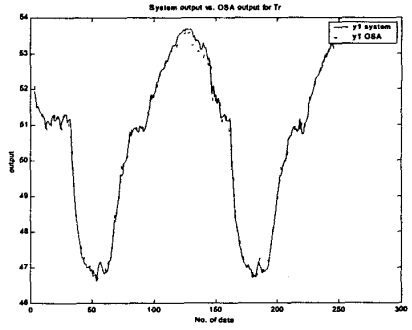

Figure 6 Cross validation for $y_1(t)$ using data set 2

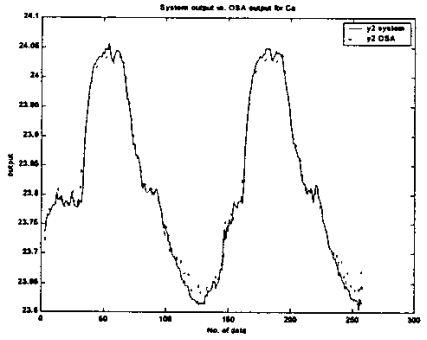

Figure 7 Cross validation for $y_2(t)$ using data set 2

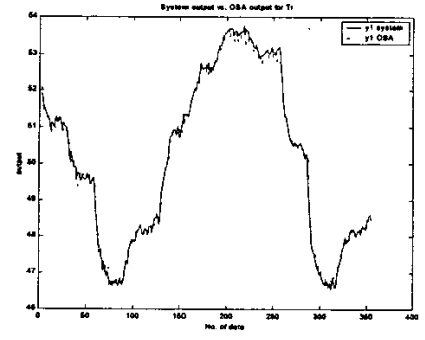

Figure 8 Cross validation for $y_1(t)$ using data set 3

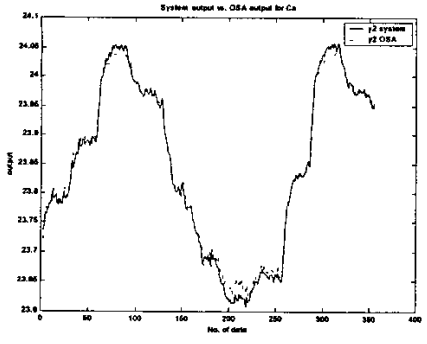

Figure 9 Cross validation for $y_2(t)$ using data set 3